

GenCore version 5.1.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1361.09 Seconds  
(without alignments)  
15778.007 Million cell updates/sec

Title: US-09-497-967-1

Perfect score: 1326

Sequence: 1 atgaataataattttatt.....ttattttttttattttattg 1326

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hci:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hci:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	404.4	30.5	658	B0135057	B0135057 INIT1_2_G
c 2	389.4	29.4	607	B0134912	B0134912 INIT1_1_F
c 3	367.6	27.7	602	B0135164	B0135164 INIT1_4_B
c 4	366.6	27.6	590	B0135179	B0135179 INIT1_4_C
c 5	317	23.9	502	B0134889	B0134889 INIT1_1_D
c 6	316.6	23.9	675	B0135196	B0135196 INIT1_4_E

c 7	308.2	23.2	445	14	B0134871	B0134871
c 8	294.4	22.2	419	14	B0135036	INIT1_1_B
c 9	280.6	21.2	661	14	B0135189	INIT1_2_D
c 10	263.8	19.9	599	14	B0134821	B0134821 INIT1_4_D
c 11	249.2	18.8	592	14	B0134985	INIT1_2_G
c 12	240.8	18.2	538	14	B0134810	B0134810 INIT1_2_D
c 13	237.4	17.9	631	14	B0134827	B0134827 INIT1_4_C
c 14	236.6	17.8	630	14	B0134905	B0134905 INIT1_4_E
c 15	227.4	17.1	687	14	B0135168	B0135168 INIT1_1_F
c 16	205.6	15.5	622	14	B0134798	B0134798 INIT1_4_B
c 17	202.6	15.4	540	14	B0134879	INIT1_1_C
c 18	196.4	14.8	523	14	B0134970	B0134970 INIT1_3_E
c 19	179.6	13.5	560	14	B0135129	B0135129 INIT1_2_D
c 20	144.2	10.9	514	14	B0134761	B0134761 INIT1_3_F
c 21	99.8	7.5	210	14	B0134900	B0134900 INIT1_3_F
c 22	86.6	6.5	150	14	B0135114	B0135114 INIT1_1_E
c 23	72	5.4	978	17	CNS040R1	AL259254 Tetraodon
c 24	71	5.4	805	17	CNS04RW2	AL259254 Tetraodon
c 25	70	5.3	747	13	EG918691	AL304427 Tetraodon
c 26	67.2	5.1	572	17	CNS043SN	BC918691 602818643
c 27	63.8	4.8	938	17	CNS07CG2	AL273200 Tetraodon
c 28	63.6	4.8	590	17	CNS03M2	AL439128 T7 end of
c 29	61.4	4.6	450	17	FR0025683	AL250244 Tetraodon
c 30	61	4.6	711	13	BM588321	AL018519 F. rubripe
c 31	60	4.5	526	17	AZ312601	BM588321 170006873
c 32	59.2	4.5	773	17	CNS01VTG	AZ312601 IM0028104
c 33	58.8	4.4	935	17	CNS033DG	AL169549 Tetraodon
c 34	58.8	4.4	536	17	FR0036552	AL25985 Tetraodon
c 35	58.8	4.4	927	17	CNS01J4S	AL124061 Fugu rubr
c 36	58.8	4.4	932	17	CNS01G4S	AL146589 Anopheles
c 37	58.4	4.4	787	13	BJ282421	AL142662 Anopheles
c 38	58.4	4.4	576	9	AA754683	BJ282421 BJ282421
c 39	58.2	4.4	735	17	CNS04NSK	AA754683 vu20e10_r
c 40	58.2	4.4	947	17	CNS01IS7	AL299119 Tetraodon
c 41	58	4.4	699	13	BM630395	AL146136 Anopheles
c 42	57.4	4.3	1101	17	CNS0039G	BM630395 170006875
c 43	57.4	4.3	650	17	AZ573029	AL063921 Drosophila
c 44	57.2	4.3	1002	17	CNS01NG1	AZ573029 312PVG08
c 45	57.2	4.3				AL151835 Anopheles

ALIGNMENTS

RESULT 1  
B0135057/c  
LOCUS  
DEFINITION  
B0135057 658 bp mRNA linear EST 23-APR-2002  
multifiliis cdna, mRNA sequence.  
ACCESSION  
B0135057  
VERSION  
B0135057.1 GI:20261156  
KEYWORDS  
EST.  
SOURCE  
Ichthyophthirius multifiliis.  
ORGANISM  
Ichthyophthirius multifiliis  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Ophryoglenina; Ichthyophthirius.  
REFERENCE  
1 (bases 1 to 658)  
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,  
Dickerson, H., Lin, T.-L. and Pratt, L.H.  
AUTHORS  
An EST database for Ichthyophthirius multifiliis (G5 isolate)  
TITLE  
Unpublished (2002)  
JOURNAL  
Contact: Cordonnier-Pratt MM  
COMMENT  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector, and regions  
below Phred quality 16. The threshold for highest quality sequence  
is 20.  
Seq primer: T7  
High quality sequence start: 67

RESULT 2					
BQI34912/c					
LOCUS	BQI34912	607 bp	mRNA	linear	EST 22-APR-2002
DEFINITION	INIT1_1_F12_b1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis CDNA, mRNA sequence.				
ACCESSION	BQI34912				



source		1. .502		/organism="Ichthyophthirius multifiliis"	
		/strain="G5"			
		/db_xref="taxon:5932"			
		/clone_lib="G5 trophont cDNA (INIT1)"			
		/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."			
BASE COUNT		185 a	80 c	70 g	167 t
ORIGIN					
Query Match		23.9%	Score 317;	DB 14;	Length 502;
Best Local Similarity		84.6%	Pred. No. 6.9e-58;		
Matches 356;		Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;
QY	906	CACATAATGTTCTTAATGCACTGCTAATTAATTTTAAAGGTAATTCGAAGCAGGTAA	965		
DB	500	CTCATAATGTTCTTAATGCTAAAGCTGGCTTTTACTAAATAGTAATTCGAAGCAGGTAA	441		
QY	966	AAATTAATGTTTAAAGTGTCCAGTAAGTAAATACCTCCAGCATCTCCAGGTAATAC	1025		
DB	440	AAATTAATGCAATAAGTGTGAGTAAGTAAATCTGGTTCAGCATCTCTCCAGGTAATAG	381		
QY	1026	TGCTACTTAAAGCCACATAATGTTTGACACATGTCCTGGTGTACAGTACTTGATGATGG	1085		
DB	380	TGCTACTTCAGCCACATAATGTTTAAAGCAATGGCTGCTGTACAGTGGTGTGATGATGG	321		
QY	1086	AAATCAACTAATTTTGTAGCTTCGCAACTGAATGTACTAAATGTTCTGCTGGCTTTT	1145		
DB	320	TACATCAACTAATTTTGTAGCTTTTACAGAGTGAATGTACTAAATGTTAGGCTACTTTTA	261		
QY	1146	TGATCAAAACAACTGGTTTACAGCAGGTACTGATACATGATGATGATGATGATGATGATG	1205		
DB	260	TGATCAAAACAACTGGTTTTCAGAGGAGTACTGATACATGATGATGATGATGATGATGATG	201		
QY	1206	ATTAACTTCTGGTGCCACAGCTAAAGTATATGCTGAAGTACTCAAAAGTAAATGCGC	1265		
DB	200	ATTAACTTCTGGTGCTACAGCTAAAGTATATGCTGAAGTACTCAAAAGTAAATGCGC	141		
QY	1266	CTCCACTACTTCGGTAAATTTTATCGAATTTCTTATTTATTTATTTCTTCTTATTTATTT	1325		
DB	140	CAGTTCCTACTTCGCAAAATTTTATCAATGCTCTTAATTTATTTCTTCTTCTTCTTCTT	81		
QY	1326	G 1326			
DB	80	G 80			
RESULT 6					
BQ135196/c					
LOCUS		675 bp mRNA linear EST 22-APR-2002			
DEFINITION		INIT1.4.E06.g1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis			
ACCESSION		BQ135196			
VERSION		BQ135196.1			
KEYWORDS		EST.			
SOURCE		GI:20261295			
ORGANISM		Ichthyophthirius multifiliis.			
REFERENCE		1 (bases 1 to 675)			
AUTHORS		Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,			
TITLE		Dickerson, H., Lin, T.-L. and Pratt, L.H.			
JOURNAL		An EST database for Ichthyophthirius multifiliis (G5 isolate)			
COMMENT		Unpublished (2002)			
CONTACT		Contact: Cordonnier-Pratt MM			
LABORATORY		Laboratory for Genomics and Bioinformatics			
UNIVERSITY		The University of Georgia, Department of Plant Biology			
BUILDING		Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA			
TEL		Tel: 706 542 1860			
FAX		Fax: 706 583 0210			
EMAIL		Email: mmpratt@uga.edu			
SEQUENCES		Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.			
PRIMER		Seq primer: JEN REV			
STOP		High quality sequence stop: 474			
POLYA-YES		Location/Qualifiers			
FEATURES					
Query Match		27.6%	Score 366.6;	DB 14;	Length 590;
Best Local Similarity		81.8%	Pred. No. 1.6e-68;		
Matches 423;		Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;
QY	810	AGGTGCTTAAGCTAATTTAGCCACATATGAGTACTTATGTCACACTGGCACTCAAT	869		
DB	590	AGGTGCTTGGAGCTAATTTAGCCGATATGTCACACTGAATGCTGCTGGCACTCTTGT	531		
QY	870	TCAACAGGAGTGACATGTTTTAGTAAATTCATCCACATAATGTTCTTAATGCAATGCG	929		
DB	530	TACAGCGGAGTAACCTACTTATGCTATGCTACTCTCATATGTTGTTAATGTAAGC	471		
QY	930	TAATTAATGTTTAAATGTAATTTGCAAGCAGGTAAAGTAAATGTTTAAAGTGTCCAGT	989		
DB	470	TGGCTTTTACTAAAATAGTAATTTGCAAGCAGGTAAAGTAAATGCAATAGTGTGCGAT	411		
QY	990	AAATTAATGCTTCCAGCAGTGTCCAGGTAATGCTACTTAAAGCCACATAATGTTT	1049		
DB	410	AAATTAATGCTTCCAGCAGTGTTCAGGTAATGCTACTTTCAGCCACATAATGTTA	351		
QY	1050	GACCCATGCTGCTGGTGTACAGTACTTGTATGATGGACATCAACTAATTTGTAGCTTC	1109		
DB	350	AAAGATTCGCCCTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	291		
QY	1110	CGCACTGAATGCTACTAATGTTCTGCTGGCTTTTTCATCAAAACAACTGGTTTAC	1169		
DB	290	AGCAAGTGAATGCTACTAATGTTGAGGCACTTTTATGATCAAAACAACTGGTTTGC	231		
QY	1170	AGCAGTACTGATACATGCTACTGAATGCTACTAAATAATTAATCTGTCGTCACAGCTAA	1229		
DB	230	AGCAGTACTGATACATGCTACTGAATGTTCTAAATAATTAATCTGTCGTCACAGCTAA	171		
QY	1230	AGTATATGCTGAAGTACTCAAAAGTATATGATGATGATGATGATGATGATGATGATG	1289		
DB	170	AGTATATGCTGAAGTACTCAAAAGTATATGATGATGATGATGATGATGATGATGATG	111		
QY	1290	ATCGATTTCTTATTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1326		
DB	110	ATCAATGCTCTTAAATTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	74		
RESULT 5					
BQ134889/c					
LOCUS		502 bp mRNA linear EST 22-APR-2002			
DEFINITION		INIT1.D07.bl.A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis			
ACCESSION		BQ134889			
VERSION		BQ134889.1			
KEYWORDS		EST.			
SOURCE		GI:20260988			
ORGANISM		Ichthyophthirius multifiliis.			
REFERENCE		1 (bases 1 to 502)			
AUTHORS		Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,			
TITLE		Dickerson, H., Lin, T.-L. and Pratt, L.H.			
JOURNAL		An EST database for Ichthyophthirius multifiliis (G5 isolate)			
COMMENT		Unpublished (2002)			
CONTACT		Contact: Cordonnier-Pratt MM			
LABORATORY		Laboratory for Genomics and Bioinformatics			
UNIVERSITY		The University of Georgia, Department of Plant Biology			
BUILDING		Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA			
TEL		Tel: 706 542 1860			
FAX		Fax: 706 583 0210			
EMAIL		Email: mmpratt@uga.edu			
SEQUENCES		Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.			
PRIMER		Seq primer: JEN REV			
STOP		High quality sequence stop: 474			
POLYA-YES		Location/Qualifiers			
FEATURES					



```

QY 1146 TGCATCAAAACAACTGGTTTACACAGGTACTGATCATCTACTGAATGTACTAAAA 1205
|||||
Db 204 TGCATCAAAACAACTGGTTTGCACAGGTACTGATCATCTACTGAATGTCTAAAA 145
|||||
QY 1206 ATTAACCTCTGGTGCACAGCTAAAGTATATGCTGAAGCTACTCAAAAGTATAATGGCG 1265
|||||
Db 144 ATTAACCTTTGGTGCACAGCTAAAGTATATGCTGAAGCTACTTAAAAAGCATATAATGGCG 85
|||||
QY 1266 CTCACCTACTTTCCGCTAAATTTTATCGATTTCCCTATTATTATTATTTCTTCTATT 1322
|||||
Db 84 CAGTTCACACTTTCCGCAAAATTTTATCAATGCTCTTAATATTATTATTCTTCTATT 28
|||||

RESULT 8
BQ135036/c
LOCUS
DEFINITION
BQ135036 419 bp mRNA linear EST 22-APR-2002
INIT1_2_D10.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ135036.1 GI:20261135
VERSION
EST.
KEYWORDS
Ichthyophthirius multifiliis.
SOURCE
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 419)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 306
High quality sequence stop: 419
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..419
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 140 a 74 c 73 g 132 t
ORIGIN
Query Match 22.2%; Score 294.4; DB 14; Length 419;
Best Local Similarity 85.4%; Pred. No. 4.9e-53;
Matches 328; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 943 AATGTAATTTTCGACAGGTAAAGTTAATGTTTAAAGTCCAGTAAGTAAACTACT 1002
|||||
Db 416 AATCGTAATTTTCGACAGGTAAAGTTAATGCAACAGTGTGCAGTAAGTAACACTGGT 357
|||||
QY 1003 CCAGCACATGCTCCAGGTAATCTGCTACTTTAAGCCACATATGCTTTGACCACATGCTCT 1062
|||||
Db 356 TCAGCATCTGTTCAGGTAATAGTCTACTTTCAGCCACATATGTTAAACGATTGCGCT 297
|||||
QY 1063 GCTGTACAGTACTTGATGATGGACATCAACTAATTTTGTAGCTTCGCCAATCAATGT 1122
|||||

```

```

Db 296 GCTGGTACAGTGGTGTGATGATGGTACATCACTAATTTTGTAGCTTTAGCAAGTGAATGT 237
|||||
QY 1123 ACTAAATGTTCTGCTGGCTTTTTCATCAAAACAACTGGTTTACAGCAGGTACTGTAT 1182
|||||
Db 236 ACTAAATGTTAGGCTAACTTTTATGCATCAAAACACTGTGTTTCGACAGGTACTGTAT 177
|||||
QY 1183 ACATGTACTGAATGACTTAAATAAATACTTCTGGTGCACAGCTAAAGTATATGCTGAA 1242
|||||
Db 176 CCATGTACTGAATGTTTAAAAAATACTTCCGGTGTACAGCTAAAGTATACGCGAA 117
|||||
QY 1243 GCTACTCAAAAGTATATGCGCTCCACTACTTTCGCTAAATTTTATCGATTTCTCTTA 1302
|||||
Db 116 GCTACTTAAAAAGCATATAATGCGCAGTTCCTACTTTCGCAAAATTTTATCAATGCCCTTA 57
|||||
QY 1303 TTATTTATTTCTTCTTATTTATTG 1326
|||||
Db 56 ATATTATTTCTTCTTATTTGTTG 33
|||||

RESULT 9
BQ135189
LOCUS
DEFINITION
BQ135189 661 bp mRNA linear EST 22-APR-2002
INIT1_4_D09.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION
BQ135189.1 GI:20261288
VERSION
EST.
KEYWORDS
Ichthyophthirius multifiliis.
SOURCE
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 661)
Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL
Unpublished (2002)
COMMENT
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 34
High quality sequence stop: 661
POLYA=No.

FEATURES
source
Location/Qualifiers
1..661
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 197 a 127 c 124 g 213 t
ORIGIN
Query Match 21.2%; Score 280.6; DB 14; Length 661;
Best Local Similarity 66.3%; Pred. No. 4.2e-50;
Matches 437; Conservative 0; Mismatches 189; Indels 33; Gaps 1;

QY 448 GTTTTGTGCTGCTGCTCCGCTGCAGGTGTTGCTGCGCTTACTAGTTAATGTACTCT 507
|||||

```











Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT	179 a	120 c	118 g	213 t
ORIGIN				
Query Match	17.8%; Score 236.6; DB 14; Length 630;			
Best Local Similarity	65.5%; Pred. No. 1.1e-40;			
Matches	416; Conservative	0; Mismatches	174; Indels	45; Gaps
				3;
Qy	2	TGAATATATATTTATTAATTTATTTCTTTTATTTATTAATGAATTAAGAGCTG	61	
Db	7	TGTCGTTAATATTTAATATTTTGAATTTCTTTATTTATTAATGAATTAAGAGCTG	66	
Qy	62	TTCCATGTCTGATGGTACTTAGACTCAAGCTGGATGACGTAGTGGTCTCTGATC	121	
Db	67	TTAATTGCTCAATGGTCTGCAATTTGCAATGGATAATCTGATACAGGAGCTGCAGATA	126	
Qy	122	TTGGTACTGTGTTAATTCGACACCTAATTTTACTATAATGGTGGTCTCTTAAGGAG	181	
Db	127	TAAATACCTTGTAATCTCTGCTAAACACCTTTTACTTTAATGGTGGTAACTCGAGGTC	186	
Qy	182	AAGCTAATGTTAATTAACCTTTGCGAGCAATAATGCTGCTAGAGGTATATGTGTACCAT	241	
Db	187	AGGCTCTGGTCTGTACAAATC-----AATCCAGGTGTTAGTCAGTGCATAGCTT	237	
Qy	242	GCCAAATAACAGAGTAGGCTCTGTTACCAATGCAGGTGACTTACTACTTATGCCACAT	301	
Db	238	GCCAAATACAAAGCGGATTTCTCAACACAGATAAGTGGTGGTATCTAATTTAGCCGCT	297	
Qy	302	AATGCAGTACTTAATCTCTACTGCGACCTGATGATGGAGTGCAGATGTTTTTG	361	
Db	298	AATGTAGCAACTATGTCTCTGGCAGCTGCGAGTGAAGATGGA---TCACCTACTTTTA	354	
Qy	362	ATAGATCAGCGCGATAATGTGTTAAATGCAACCTAACTTTTACTATATAGTGGTCTC	421	
Db	355	CTTAATCCCTCACATAATGTGTTAATGTAAACCTAACTTTTACTTTAATGGTGGTAATC	414	
Qy	422	CTTAAGGTGAAGCTCTCGGGTTAA-----G	448	
Db	415	CTACAGTACAGGCTCTGGTGGGATAATTCATGATCCAACTTAATGATGCAATCTCG	474	
Qy	449	TTTTTGTCTGTGTGTCGCGCTGCGAGTGTGCTGCCGTTACTAGTTAATGTGACCTT	508	
Db	475	ATCTTGCTAATAATCTGAAGTTCCTAATGTTTCTAGCCCTAATGTTAATCGTAGCTT	534	
Qy	509	GCCAACTAAACAAAGATTTCTCTGCGCACTGCAGTGCCTAAGCTAATTTAGCCACAT	568	
Db	535	GCTAAGTAAACAAGCTCTGATCTCAATTAAGACCGAGTGTAGGCTAATTTAGCCACAT	594	
Qy	569	AATGTAGCAATTAATGTCCTACTGGCACTGTACTT	603	
Db	595	AATGTAGCAATGAATGTCCTACTGGCACTGTACTT	629	

RESULT 15  
B0135168  
LOCUS  
DEFINITION  
INIT\_4\_B09.g1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA, mRNA sequence.  
ACCESSION  
B0135168  
VERSION  
B0135168.1  
KEYWORDS  
EST  
SOURCE  
Ichthyophthirius multifiliis.  
ORGANISM  
Ichthyophthirius multifiliis  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.  
REFERENCE  
1 (bases 1 to 687)  
AUTHORS  
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.  
TITLE  
An EST database for Ichthyophthirius multifiliis (G5 isolate)  
JOURNAL  
Unpublished (2002)

COMMENT

Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: T7  
High quality sequence start: 90  
High quality sequence stop: 687  
POLYA=No.

FEATURES

Source  
1..687  
/organism="Ichthyophthirius multifiliis"  
/strain="G5"  
/db\_xref="taxon:5932"  
/clone\_lib="G5 trophont cDNA (INIT1)"  
/note="vector: pBluescript SK(-) from Lambda Zap II;  
Site 1: EcoRI; Site 2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.  
Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT 194 a 137 c 130 g 226 t

ORIGIN

Query Match 17.1%; Score 227.4; DB 14; Length 687;  
Best Local Similarity 62.6%; Pred. No. 1e-38;  
Matches 429; Conservative 0; Mismatches 211; Indels 45; Gaps 3;  
Qy 108 AGTGCTGCTGATCTTGGTACTTGTAAATTTGCAGACCTAATTTTACTATAATGGTGG 167  
Db 11 AGAGCTCGAGATATAAATCTGTACTCATTTCTTAAACACACTTTTACTTTAATGGTGG 70  
Qy 168 TGGTCTTAAGGAGAGCTAATGGTAATTAACCTTTCGCGCAATAATGCTGCTAGAGG 227  
Db 71 TAATCTCGCAGGTGCTGGTCTGTACAAATTC-----AATCCAGGTGTTAG 121

Qy 228 TATATGTGTACCATGCAATAAACAAGAGTAGGCTCTGTACCAATGCGAGGTGACTTAGC 287  
Db 122 TCAGTGCATACCTTGCACAGTACACAAAGCCGATTCTCAACACAGATAAGGTGGTATGC 181  
Qy 288 TACTTTAGCCACATAATGCAAGTACTTAATGTCCTACTGGCACTGCACTTGATGATGGAGT 347  
Db 182 TAATTTAGCCGCATAATGTAGCAACTTATGCTGCTGGCACTGCACTTGAAGATGGA-- 239  
Qy 348 GACAGATGTTTTTGATAGATCAGCCGCAATAATGTTAAATGCAAACTTAACCTTTTACTA 407  
Db 240 -TCACCTACTTTTACTTAATCCCTCACATAATGTTAATGTTAAACCTTAACCTTTTACTT 298  
Qy 408 TAATGGTGGTCTCTCCCTTAAGGTGAAGCTCTCTGGCGTTTAA----- 447  
Db 299 TAATGGTGGTAAATCCCTACAGGTGAGGCTCTCTGGTCTGGATAATTCGATCCAACTTAAT 358  
Qy 448 -----GTTTTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 494  
Db 359 GATTGCAAACTCTGATCTTCTGCTAATATCTGAAAGTTCCTAATGTTTCTAGCCCTAATGG 418  
Qy 495 TTAATGTGTACCTTGCCAACTTAACAAAAAGATTTCTCTGCGCACTGCAAGGTGCCTTAAGC 554  
Db 419 TTAATGCGGTAGCTTGAAGTAAACAAGTCTGATTCATTAAGACAGGAGGTGCTTAGGC 478  
Qy 555 TAAATTTAGCCACATAATGTAGCAATTAATGTCCTACTGGCACTGCTACTGATGATGGAGT 614  
Db 479 TAAATTTAGCCACATAATGTAAACAATGAATGCTCTACTGGCACTGCTATTCAAGACGAGC 538  
Qy 615 GACACTGTTTTTAAATACATCAGCCACATTAATGTTAAATGATGAGACCTTAACCTTTTACTA 674  
Db 539 AATATTATTATTACTTAATCAATCTCATATGTTACTTTTTTGTAAAGTGCACCTTTTACTT 598

Search completed: February 16, 2003, 22:24:44  
Job time : 1372.09 secs

